

SEQUENCE LISTING

<110> Mahajan, Pramod B.

<120> Maize Orthologues of Bacterial RuvB:
cDNAs and Uses Thereof

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<150> US 60/144,112

<151> 1999-07-16

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<212> DNA

<213> Zea mays

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<221> CDS

<222> (85)...(1449)

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Ser Lys Lys Gln Arg Ile Ala Thr His Thr His Ile Lys Gly Leu Gly	
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Leu Asp Ala Asn Gly Met Ala Ile Ala Leu Ala Ala Gly Phe Val Gly	
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cag tcg gcg gcg cgc gag gcg gcc ggg ctg gcg gtc gac atg att cgc	255
Gln Ser Ala Ala Arg Glu Ala Ala Gly Leu Ala Val Asp Met Ile Arg	
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Gln Lys Lys Met Ala Gly Arg Ala Val Leu Leu Val Gly Pro Pro Ala	
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acg ggc aag acg gcg cta gcg ctc ggc ata gcc cag gag ctc ggc agc	351
Thr Gly Lys Thr Ala Leu Ala Leu Gly Ile Ala Gln Glu Leu Gly Ser	
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aag gtc cct ttc tgc cct atg gta gga tca gaa gtg tac tcc tcg gag	399
Lys Val Pro Phe Cys Pro Met Val Gly Ser Glu Val Tyr Ser Ser Glu	
90 95 100 105	
gtc aag aaa act gag gtg ctg atg gaa aat ttc cgt aga gct ata ggt	447
Val Lys Lys Thr Glu Val Leu Met Glu Asn Phe Arg Arg Ala Ile Gly	
110 115 120	

004090" DT568560

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			125				130						135			
ctt	tcc	cca	gaa	gag	gct	gag	agt	aca	act	ggt	gga	tat	gca	aaa	agc	543
Leu	Ser	Pro	Glu	Glu	Ala	Glu	Ser	Thr	Thr	Gly	Gly	Tyr	Ala	Lys	Ser	
			140				145						150			
att	agc	cat	gta	atc	atc	agc	tta	aag	act	gtt	aaa	ggg	act	aag	caa	591
Ile	Ser	His	Val	Ile	Ile	Ser	Leu	Lys	Thr	Val	Lys	Gly	Thr	Lys	Gln	
			155				160						165			
ctg	aag	tta	gat	tct	tca	att	tat	gat	gct	ctg	atc	aag	gaa	aag	gtg	639
Leu	Lys	Leu	Asp	Ser	Ser	Ile	Tyr	Asp	Ala	Leu	Ile	Lys	Glu	Lys	Val	
			170				175						180			185
gca	gtg	ggg	gat	gtt	ata	tac	att	gaa	gca	aat	agt	gga	gca	gtg	aaa	687
Ala	Val	Gly	Asp	Val	Ile	Tyr	Ile	Glu	Ala	Asn	Ser	Gly	Ala	Val	Lys	
			190				195						200			
aga	gtt	ggg	aga	tgt	gat	tct	ttt	gct	aca	gaa	tac	gat	ctt	gaa	gct	735
Arg	Val	Gly	Arg	Cys	Asp	Ser	Phe	Ala	Thr	Glu	Tyr	Asp	Leu	Glu	Ala	
			205				210						215			
gaa	gaa	tat	gtt	cct	atc	ccc	aaa	ggg	gaa	gtc	cat	aag	aaa	aaa	gaa	783
Glu	Glu	Tyr	Val	Pro	Ile	Pro	Lys	Gly	Glu	Val	His	Lys	Lys	Lys	Glu	
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ata	gtg	cag	gat	gtc	aca	ctt	cat	gac	ctt	gat	gca	gca	aat	gct	cag	831
Ile	Val	Gln	Asp	Val	Thr	Leu	His	Asp	Leu	Asp	Ala	Ala	Asn	Ala	Gln	
			235				240						245			
cca	caa	ggg	ggc	caa	gat	att	ttg	tcc	ctt	atg	ggc	cag	atg	atg	aaa	879
Pro	Gln	Gly	Gly	Gln	Asp	Ile	Leu	Ser	Leu	Met	Gly	Gln	Met	Met	Lys	
			250				255						260			265
cca	cga	aag	act	gaa	atc	acc	gaa	aaa	cta	cgc	caa	gaa	att	aat	aag	927
Pro	Arg	Lys	Thr	Glu	Ile	Thr	Glu	Lys	Leu	Arg	Gln	Glu	Ile	Asn	Lys	
			270				275						280			
gtg	gta	aat	aga	tat	atc	gat	gaa	gga	att	gca	gag	ctt	gta	cct	ggg	975
Val	Val	Asn	Arg	Tyr	Ile	Asp	Glu	Gly	Ile	Ala	Glu	Leu	Val	Pro	Gly	
			285				290						295			
gtt	tta	ttc	att	gac	gag	gtc	cac	atg	ttg	gat	atc	gaa	tgt	ttt	tct	1023
Val	Leu	Phe	Ile	Asp	Glu	Val	His	Met	Leu	Asp	Ile	Glu	Cys	Phe	Ser	
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tat	ctt	aac	cgt	gca	ttg	gag	agc	cca	tta	tca	cca	att	gtg	ata	ctt	1071
Tyr	Leu	Asn	Arg	Ala	Leu	Glu	Ser	Pro	Leu	Ser	Pro	Ile	Val	Ile	Leu	
			315				320						325			
gct	acg	aat	agg	gga	ata	tgt	aat	gta	aga	gga	act	gat	atg	aca	agt	1119
Ala	Thr	Asn	Arg	Gly	Ile	Cys	Asn	Val	Arg	Gly	Thr	Asp	Met	Thr	Ser	
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cca	cat	ggg	ata	cca	gtg	gat	ctt	cta	gat	agg	ttg	gtg	att	att	cgg	1167
Pro	His	Gly														

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 Thr Glu Thr Tyr Gly Pro Thr Glu Met Ile Gln Ile Leu Ala Ile Arg
 365 370 375

gca caa gtg gag gac att gat atg gat gaa gaa agt ctt gct tat tta 1263
 Ala Gln Val Glu Asp Ile Asp Met Asp Glu Glu Ser Leu Ala Tyr Leu
 380 385 390

ggc gag atc gga cag cag aca tct tta aga cat gct att caa ttg ata 1311
 Gly Glu Ile Gly Gln Gln Thr Ser Leu Arg His Ala Ile Gln Leu Ile
 395 400 405

tca cct gcc agc gtg gtc tca aag act aat gga aga gag aaa ata tgc 1359
 Ser Pro Ala Ser Val Val Ser Lys Thr Asn Gly Arg Glu Lys Ile Cys
 410 415 420 425

aag gct gat ctc gag gaa gtc agt ggg ctc tat ttg gat gcc aaa tcc 1407
 Lys Ala Asp Leu Glu Glu Val Ser Gly Leu Tyr Leu Asp Ala Lys Ser
 430 435 440

tcg gct cgg ctg ctc cag gag caa caa gaa aga tac atc acc 1449
 Ser Ala Arg Leu Leu Gln Glu Gln Glu Glu Arg Tyr Ile Thr
 445 450 455

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 <213> Zea mays

<400> 2

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 Ile Ala Leu Ala Ala Gly Phe Val Gly Gln Ser Ala Ala Arg Glu Ala
 35 40 45
 Ala Gly Leu Ala Val Asp Met Ile Arg Gln Lys Lys Met Ala Gly Arg
 50 55 60
 Ala Val Leu Leu Val Gly Pro Pro Ala Thr Gly Lys Thr Ala Leu Ala
 65 70 75 80
 Leu Gly Ile Ala Gln Glu Leu Gly Ser Lys Val Pro Phe Cys Pro Met
 85 90 95
 Val Gly Ser Glu Val Tyr Ser Ser Glu Val Lys Lys Thr Glu Val Leu
 100 105 110
 Met Glu Asn Phe Arg Arg Ala Ile Gly Leu Arg Ile Lys Glu Asn Lys
 115 120 125
 Glu Val Tyr Glu Gly Glu Val Thr Glu Leu Ser Pro Glu Glu Ala Glu
 130 135 140
 Ser Thr Thr Gly Gly Tyr Ala Lys Ser Ile Ser His Val Ile Ile Ser
 145 150 155 160
 Leu Lys Thr Val Lys Gly Thr Lys Gln Leu Lys Leu Asp Ser Ser Ile
 165 170 175
 Tyr Asp Ala Leu Ile Lys Glu Lys Val Ala Val Gly Asp Val Ile Tyr
 180 185 190

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Ile Glu Ala Asn Ser Gly Ala Val Lys Arg Val Gly Arg Cys Asp Ser
 195 200 205
 Phe Ala Thr Glu Tyr Asp Leu Glu Ala Glu Glu Tyr Val Pro Ile Pro
 210 215 220
 Lys Gly Glu Val His Lys Lys Lys Glu Ile Val Gln Asp Val Thr Leu
 225 230 235 240
 His Asp Leu Asp Ala Ala Asn Ala Gln Pro Gln Gly Gly Gln Asp Ile
 245 250 255
 Leu Ser Leu Met Gly Gln Met Met Lys Pro Arg Lys Thr Glu Ile Thr
 260 265 270
 Glu Lys Leu Arg Gln Glu Ile Asn Lys Val Val Asn Arg Tyr Ile Asp
 275 280 285
 Glu Gly Ile Ala Glu Leu Val Pro Gly Val Leu Phe Ile Asp Glu Val
 290 295 300
 His Met Leu Asp Ile Glu Cys Phe Ser Tyr Leu Asn Arg Ala Leu Glu
 305 310 315 320
 Ser Pro Leu Ser Pro Ile Val Ile Leu Ala Thr Asn Arg Gly Ile Cys
 325 330 335
 Asn Val Arg Gly Thr Asp Met Thr Ser Pro His Gly Ile Pro Val Asp
 340 345 350
 Leu Leu Asp Arg Leu Val Ile Ile Arg Thr Glu Thr Tyr Gly Pro Thr
 355 360 365
 Glu Met Ile Gln Ile Leu Ala Ile Arg Ala Gln Val Glu Asp Ile Asp
 370 375 380
 Met Asp Glu Glu Ser Leu Ala Tyr Leu Gly Glu Ile Gly Gln Gln Thr
 385 390 395 400
 Ser Leu Arg His Ala Ile Gln Leu Ile Ser Pro Ala Ser Val Val Ser
 405 410 415
 Lys Thr Asn Gly Arg Glu Lys Ile Cys Lys Ala Asp Leu Glu Glu Val
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 Met Arg Ile Glu Glu Val Gln
 1 5

 tcg acc tcg aag aag cag cgc atc gcc acc cac acc cac atc aag gga 162
 Ser Thr Ser Lys Lys Gln Arg Ile Ala Thr His Thr His Ile Lys Gly
 10 15 20

 ctc ggc ctc gac gcc aat ggg atg gcg att gcg ttg gcg gcg ggg ttc 210
 Leu Gly Leu Asp Ala Asn Gly Met Ala Ile Ala Leu Ala Ala Gly Phe
 25 30 35

 gtg ggc cag gcg gcg gcg cgc gag gcg gcc ggg ctg gcg gtc gac atg 258
 Val Gly Gln Ala Ala Ala Arg Glu Ala Ala Gly Leu Ala Val Asp Met
 40 45 50 55

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ccc gcc acg ggc aag acg gcg cta gcg ctc ggc ata gcc cag gag ctc Pro Ala Thr Gly Lys Thr Ala Leu Ala Leu Gly Ile Ala Gln Glu Leu 75 80 85	354
ggc agc aag gtc cct ttc tgt cct atg gta gga tca gaa gtg tac tcc Gly Ser Lys Val Pro Phe Cys Pro Met Val Gly Ser Glu Val Tyr Ser 90 95 100	402
tcg gag gtc aag aaa act gag gtg ctg atg gaa aat ttc cgt aga gct Ser Glu Val Lys Lys Thr Glu Val Leu Met Glu Asn Phe Arg Arg Ala 105 110 115	450
ata ggt ttg cgt ata aag gaa aac aaa gag gtt tat gaa gga gag gtt Ile Gly Leu Arg Ile Lys Glu Asn Lys Glu Val Tyr Glu Gly Glu Val 120 125 130 135	498
act gaa ctt tcc cca gaa gag gct gag agt aca act ggt gga tat gca Thr Glu Leu Ser Pro Glu Glu Ala Glu Ser Thr Thr Gly Gly Tyr Ala 140 145 150	546
aaa agc att agc cat gta atc atc agc tta aag act gtt aaa ggg act Lys Ser Ile Ser His Val Ile Ile Ser Leu Lys Thr Val Lys Gly Thr 155 160 165	594
aag caa ctg aag tta gat tct tca att tat gat gct ctg atc aag gaa Lys Gln Leu Lys Leu Asp Ser Ser Ile Tyr Asp Ala Leu Ile Lys Glu 170 175 180	642
aag gtg gca gtg ggt gat gtt ata tac atc gaa gca aat agt gga gca Lys Val Ala Val Gly Asp Val Ile Tyr Ile Glu Ala Asn Ser Gly Ala 185 190 195	690
gtg aaa aga gtt ggt aga tgt gat tct ttt gct aca gaa tac gat ctt Val Lys Arg Val Gly Arg Cys Asp Ser Phe Ala Thr Glu Tyr Asp Leu 200 205 210 215	738
gaa gct gaa gag tat gtt cct atc ccc aaa ggt gaa gtc cat aag aaa Glu Ala Glu Glu Tyr Val Pro Ile Pro Lys Gly Glu Val His Lys Lys 220 225 230	786
aaa gaa att gtg cag gat gtc aca ctt cat gac ctt gat gca gca aat Lys Glu Ile Val Gln Asp Val Thr Leu His Asp Leu Asp Ala Ala Asn 235 240 245	834
gct cag cca caa ggt ggc caa gat att ttg tcc ctt atg ggc cag atg Ala Gln Pro Gln Gly Gly Gln Asp Ile Leu Ser Leu Met Gly Gln Met 250 255 260	882
atg aaa cca cga aag act gaa atc acc gaa aaa cta cgc caa gaa att Met Lys Pro Arg Lys Thr Glu Ile Thr Glu Lys Leu Arg Gln Glu Ile 265 270 275	930
aat aag gtg gta aat aga tat atc gat gaa gga att gca gag ctt gta Asn Lys Val Val Asn Arg Tyr Ile Asp Glu Gly Ile Ala Glu Leu Val 280 285 290 295	978

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Pro Gly Val Leu Phe Ile Asp Glu Val His Met Leu Asp Ile Glu Cys
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Phe Ser Tyr Leu Asn Arg Ala Leu Glu Ser Pro Leu Ser Pro Ile Val
315 320 325

ata ctt gct aca aat agg gga ata tgt aat gta aga gga act gat atg 1122
Ile Leu Ala Thr Asn Arg Gly Ile Cys Asn Val Arg Gly Thr Asp Met
330 335 340

aca agt cca cat ggt ata ccg gtg gat ctt cta gat agg ctg gtg att 1170
Thr Ser Pro His Gly Ile Pro Val Asp Leu Leu Asp Arg Leu Val Ile
345 350 355

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Ile Arg Thr Glu Thr Tyr Gly Pro Thr Glu Met Ile Gln Ile Leu Ala
360 365 370 375

atc cga gca caa gtg gag gag att gat atg gat gaa gaa agt ctt gct 1266
Ile Arg Ala Gln Val Glu Glu Ile Asp Met Asp Glu Glu Ser Leu Ala
380 385 390

tat tta ggc gag atc gga cag cag aca tct ttg aga cat gct att caa 1314
Tyr Leu Gly Glu Ile Gly Gln Gln Thr Ser Leu Arg His Ala Ile Gln
395 400 405

ttg ata tca cct gcc agc gtg gtc tca aag act aat gga aga gag aaa 1362
Leu Ile Ser Pro Ala Ser Val Val Ser Lys Thr Asn Gly Arg Glu Lys
410 415 420

atc tgc aag gct gat ctc gag gaa gtc agt ggg ctc tat ttg gat gcc 1410
Ile Cys Lys Ala Asp Leu Glu Glu Val Ser Gly Leu Tyr Leu Asp Ala
425 430 435

aaa tcc tcg gct cgg ctg ctc cag gag caa caa gaa aga tac atc acc 1458
Lys Ser Ser Ala Arg Leu Leu Gln Glu Gln Gln Glu Arg Tyr Ile Thr
440 445 450 455

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taaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1912

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35 40 45
Ala Gly Leu Ala Val Asp Met Ile Arg Gln Lys Lys Met Ala Gly Arg

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Leu Gly Ile Ala Gln	Leu Gly Ser Lys	Val Pro Phe Cys Pro Met
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Val Gly Ser Glu Val Tyr	Ser Ser Glu Val Lys	Lys Thr Glu Val Leu
100	105	110
Met Glu Asn Phe Arg Arg	Ala Ile Gly Leu Arg	Ile Lys Glu Asn Lys
115	120	125
Glu Val Tyr Glu Gly Glu	Val Thr Glu Leu Ser	Pro Glu Glu Ala Glu
130	135	140
Ser Thr Thr Gly Gly Tyr	Ala Lys Ser Ile Ser	His Val Ile Ile Ser
145	150	155
Leu Lys Thr Val Lys	Gly Thr Lys Gln Leu Lys	Leu Asp Ser Ser Ile
165	170	175
Tyr Asp Ala Leu Ile Lys	Glu Lys Val Ala Val	Gly Asp Val Ile Tyr
180	185	190
Ile Glu Ala Asn Ser Gly	Ala Val Lys Arg Val	Gly Arg Cys Asp Ser
195	200	205
Phe Ala Thr Glu Tyr Asp	Leu Glu Ala Glu Glu	Tyr Val Pro Ile Pro
210	215	220
Lys Gly Glu Val His Lys	Lys Lys Glu Ile Val	Gln Asp Val Thr Leu
225	230	235
His Asp Leu Asp Ala Ala	Asn Ala Gln Pro Gln	Gly Gly Gln Asp Ile
245	250	255
Leu Ser Leu Met Gly Gln	Met Met Lys Pro Arg	Lys Thr Glu Ile Thr
260	265	270
Glu Lys Leu Arg Gln Glu	Ile Asn Lys Val Val	Asn Arg Tyr Ile Asp
275	280	285
Glu Gly Ile Ala Glu Leu	Val Pro Gly Val Leu	Phe Ile Asp Glu Val
290	295	300
His Met Leu Asp Ile Glu	Cys Phe Ser Tyr Leu	Asn Arg Ala Leu Glu
305	310	315
Ser Pro Leu Ser Pro Ile	Val Ile Leu Ala Thr	Asn Arg Gly Ile Cys
325	330	335
Asn Val Arg Gly Thr Asp	Met Thr Ser Pro His	Gly Ile Pro Val Asp
340	345	350
Leu Leu Asp Arg Leu Val	Ile Ile Arg Thr Glu	Thr Tyr Gly Pro Thr
355	360	365
Glu Met Ile Gln Ile Leu	Ala Ile Arg Ala Gln	Val Glu Glu Ile Asp
370	375	380
Met Asp Glu Glu Ser Leu	Ala Tyr Leu Gly Glu	Ile Gly Gln Gln Thr
385	390	395
Ser Leu Arg His Ala Ile	Gln Leu Ile Ser Pro	Ala Ser Val Val Ser
405	410	415
Lys Thr Asn Gly Arg Glu	Lys Ile Cys Lys Ala	Asp Leu Glu Glu Val
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 <222> (82)...(1446)

<400> 5

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Met Arg Ile Glu Glu Val Gln Ser Thr Ser	
1 5 10	
aag aag cag cgc atc gcc acc cac act cac atc aag ggc ctc ggc ctc	159
Lys Lys Gln Arg Ile Ala Thr His Thr His Ile Lys Gly Leu Gly Leu	
15 20 25	
gac gcc aat gga atg tcg atg ccg ttg gcg gcg ggg ttc gtg ggc cag	207
Asp Ala Asn Gly Met Ser Met Pro Leu Ala Ala Gly Phe Val Gly Gln	
30 35 40	
gcg gcg gcg cgc gag gcg gcc ggg ctg gcg gtc gac atg atc cgc cag	255
Ala Ala Ala Arg Glu Ala Ala Gly Leu Ala Val Asp Met Ile Arg Gln	
45 50 55	
aag aag atg gcc ggt cgc gcg ctg ctc ctt gcg ggc ccg ccc gcc acg	303
Lys Lys Met Ala Gly Arg Ala Leu Leu Leu Ala Gly Pro Pro Ala Thr	
60 65 70	
ggc aaa acg gcg cta gcg ctc ggc ata gcg cag gag ctc ggc agc aag	351
Gly Lys Thr Ala Leu Ala Leu Gly Ile Ala Gln Glu Leu Gly Ser Lys	
75 80 85 90	
gtc cca ttc tgt cct atg gta gga tca gaa gtg tac tcc tca gag gtc	399
Val Pro Phe Cys Pro Met Val Gly Ser Glu Val Tyr Ser Ser Glu Val	
95 100 105	
aag aaa act gag gtg ctg atg gaa aat ttc cgt aga gct ata ggt ttg	447
Lys Lys Thr Glu Val Leu Met Glu Asn Phe Arg Arg Ala Ile Gly Leu	
110 115 120	
cgt ata aag gaa aac aaa gag gtt tat gaa gga gag gtt att gaa ctt	495
Arg Ile Lys Glu Asn Lys Glu Val Tyr Glu Gly Glu Val Ile Glu Leu	
125 130 135	
tcc cca gaa gag gct gag agc aca act ggt gga tat gcg aaa agc att	543
Ser Pro Glu Glu Ala Glu Ser Thr Thr Gly Gly Tyr Ala Lys Ser Ile	
140 145 150	
agc cac gta atc att ggc tta aag act gtc aaa ggg act aag caa ttg	591
Ser His Val Ile Ile Gly Leu Lys Thr Val Lys Gly Thr Lys Gln Leu	
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Lys Leu Asp Pro Ser Ile Tyr Asp Ala Leu Ile Lys Glu Lys Val Ala	
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Val Gly Asp Val Ile Tyr Ile Glu Ala Asn Ser Gly Ala Val Lys Arg	
190 195 200	
gtt ggt aga tgt gat tct ttt gct aca gaa tat gat ctt gaa gct gaa	735
Val Gly Arg Cys Asp Ser Phe Ala Thr Glu Tyr Asp Leu Glu Ala Glu	
205 210 215	
gag tat gtt cct atc ccc aaa ggt gaa gtc cat aag aaa aag gaa ata	783
Glu Tyr Val Pro Ile Pro Lys Gly Glu Val His Lys Lys Lys Glu Ile	
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Gln Gly Gly Gln Asp Ile Leu Ser Leu Met Gly Gln Met Met Lys Pro	
255 260 265	
cgg aag act gaa atc acc gaa aag cta cgc caa gaa atc aat aag gtg	927
Arg Lys Thr Glu Ile Thr Glu Lys Leu Arg Gln Glu Ile Asn Lys Val	
270 275 280	
gta aac aga tat atc gac gaa gga atc gca gag ctt gta cct ggt gtt	975
Val Asn Arg Tyr Ile Asp Glu Gly Ile Ala Glu Leu Val Pro Gly Val	
285 290 295	
ttg ttc att gat gag gtc cac atg ttg gat att gaa tgc ttt tct tat	1023
Leu Phe Ile Asp Glu Val His Met Leu Asp Ile Glu Cys Phe Ser Tyr	
300 305 310	
ctt aac cgt gca ttg gag agc cca tta tca cca att gtg ata ctc gct	1071
Leu Asn Arg Ala Leu Glu Ser Pro Leu Ser Pro Ile Val Ile Leu Ala	
315 320 325 330	
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Thr Asn Arg Gly Ile Cys Asn Val Arg Gly Thr Asp Met Thr Ser Pro	
335 340 345	
cat ggt ata cca gtg gac ctt cta gat agg ttg gtg att att cgg aca	1167
His Gly Ile Pro Val Asp Leu Leu Asp Arg Leu Val Ile Ile Arg Thr	
350 355 360	
gaa aca tat ggc cct act gag atg ata cag ata ctg gct atc cga gca	1215
Glu Thr Tyr Gly Pro Thr Glu Met Ile Gln Ile Leu Ala Ile Arg Ala	
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Gln Val Glu Glu Ile Asp Ile Asp Glu Glu Ser Leu Ala Tyr Leu Gly	
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1876
 1886

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 Ala Gly Leu Ala Val Asp Met Ile Arg Gln Lys Lys Met Ala Gly Arg
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 Leu Ser Leu Met Gly Gln Met Met Lys Pro Arg Lys Thr Glu Ile Thr
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 Glu Gly Ile Ala Glu Leu Val Pro Gly Val Leu Phe Ile Asp Glu Val
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 Ser Pro Leu Ser Pro Ile Val Ile Leu Ala Thr Asn Arg Gly Ile Cys
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Met Arg Ile Glu																
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gtc Val 230	cat His	aag Lys	aaa Lys	aag Lys	gaa Glu	ata Ile 235	gtg Val	cag Gln	gat Asp	gtc Val	aca Thr 240	ctc Leu	cat His	gac Asp	ctt Leu	897
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cgc Arg	caa Gln	gaa Glu	atc Ile 280	aat Asn	aag Lys	gtg Val	gta Val	aac Asn 285	aga Arg	tat Tyr	atc Ile	gac Asp	gaa Glu 290	gga Gly	atc Ile	1041
gca Ala	gag Glu	ctt Leu	gta Val	cct Pro	ggt Gly	gtt Val	ttg Leu 300	ttc Phe	att Ile	gat Asp	gag Glu	gtc Val 305	cac His	atg Met	ttg Leu	1089
gat Asp 310	att Ile	gaa Glu	tgc Cys	ttt Phe	tct Ser	tat Tyr 315	ctt Leu	aac Asn	cgt Arg	gca Ala	ttg Leu 320	gag Glu	agc Ser	cca Pro	tta Leu	1137
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agg Arg	ttg Leu	gtg Val	att Ile 360	att Ile	cgg Arg	aca Thr	gaa Glu	aca Thr 365	tat Tyr	ggc Gly	cct Pro	act Thr	gag Glu 370	atg Met	ata Ile	1281
cag Gln	ata Ile	ctg Leu	gct Ala	atc Ile	cga Arg	gca Ala	caa Gln 380	gtg Val	gaa Glu	gag Glu	att Ile 385	gat Asp	atc Ile	gat Asp	gaa Glu	1329
gaa Glu	agt Ser 390	ctt Leu	gct Ala	tat Tyr	tta Leu	ggc Gly 395	gag Glu	atc Ile	gga Gly	cag Gln 400	cag Gln	aca Thr	tct Ser	ttg Leu	aga Arg	1377
cat His	gct Ala	att Ile	cag Gln	ttg Leu	cta Leu	tca Ser	cct Pro	gcc Ala	agc Ser	gtg Val	gtc Val	gca Ala	aag Lys	acc Thr	aac Asn	1425

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 Arg Tyr Ile Thr
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Lys	Glu	Val	Tyr	Glu	Gly	Glu	Val	Ile	Glu	Leu	Ser	Pro	Glu	Glu	Ala
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Tyr	Ile	Glu	Ala	Asn	Ser	Gly	Ala	Val	Lys	Arg	Val	Gly	Arg	Cys	Asp
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Pro	Lys	Gly	Glu	Val	His	Lys	Lys	Lys	Glu	Ile	Val	Gln	Asp	Val	Thr
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 Cys Asn Val Arg Gly Thr Asp Met Thr Ser Pro His Gly Ile Pro Val
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 Ala Lys Thr Asn Gly Arg Glu Lys Met Cys Lys Ala Asp Leu Glu Glu
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 Met Arg Ile Glu Glu Val Gln Ser Thr Ser Lys Lys Gln Arg Ile
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 Ala Thr His Thr His Ile Lys Gly Leu Gly Leu Asp Ala Asn Gly Met
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cgc gcg gtg ctc ctt gcg ggt ccg ccc gcc acg ggc aag acg gcg cta 252
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 Val Gly Ser Glu Val Tyr Ser Ser Glu Val Lys Lys Thr Glu Val Leu
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 Ile Glu Ala Asn Ser Gly Ala Val Lys Arg Val Gly Arg Cys Asp Ser
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 His Asp Leu Asp Ala Ala Asn Ala Gln Pro Gln Gly Gly Gln Asp Ile
 225 230 235

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 His Met Leu Asp Ile Glu Cys Phe Ser Tyr Leu Asn Arg Ala Leu Glu
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agc cca tta tca cca atc gtg ata ctt gct aca aat agg gga ata tgt 1020
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 Gly Ile Ala Gln Glu Leu Gly Ser Lys Val Pro Phe Cys Pro Met Val
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 Asp Ala Leu Ile Lys Glu Lys Val Ala Val Gly Asp Val Ile Tyr Ile
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 Glu Ala Asn Ser Gly Ala Val Lys Arg Val Gly Arg Cys Asp Ser Phe

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 225 230 235 240
 Ser Leu Met Gly Gln Met Met Lys Pro Arg Lys Thr Glu Ile Thr Glu
 245 250 255
 Lys Leu Arg Gln Glu Ile Asn Lys Val Val Asn Arg Tyr Ile Asp Glu
 260 265 270
 Gly Ile Ala Glu Leu Val Pro Gly Val Leu Phe Ile Asp Glu Val His
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 Asp Glu Glu Ser Leu Ala Tyr Leu Gly Glu Ile Gly Gln Gln Thr Ser
 370 375 380
 Leu Arg His Ala Ile Gln Leu Ile Ser Pro Ala Ser Val Val Ser Lys
 385 390 395 400
 Thr Asn Gly Arg Glu Lys Ile Cys Lys Ala Asp Leu Glu Glu Val Ser
 405 410 415
 Gly Leu Tyr Leu Asp Ala Lys Ser Ser Ala Arg Leu Leu Gln Glu Gln
 420 425 430
 Gln Glu Arg Tyr Ile Thr
 435

<210> 11
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide based upon an adaptor
 used for cDNA library construction and poly(dT) to
 remove clones which have a poly(A) tail but no
 cDNA insert.

<400> 11
 tcgacccacg cgtccgaaaa aaaaaaaaaa aaaaaa